

SPECIFICATION AMENDMENTS

Please amend paragraph [0050] beginning on page 8 as follows:

To address the problem of large differences in length between subsequences in a display, such as exons and introns, alternately spliced modules and large exons, or between categories of annotations, the gene product representation technique uses one or more scales within the same display. (See Figures 11, 12, 13 and 14.) (Comment on Figure 11: An EST (in orange), aligned against all transcripts (in blue) of AKT3 in the NCBI human genome annotations. The EST contains an additional exon not present in the transcripts.) (Comments on Figure 12: An EST (in orange), aligned against all transcripts (in blue) of kinase GPRK2L in the NCBI human genome annotations. The EST is missing 2 or 3 exons present in the transcripts. To “zoom in” on exon 3, the scale for that region can be altered while retaining the same scale for the rest of the view. The graphic representation of the selected region can be altered as a function of the scale. E.g., at a certain scale, the bar could be replaced with the NT or AA sequence.) (Comment on Figure 13: The sequences of Figure 11, as displayed using a single base scale for all introns and exons. Note that it is impossible to determine the relative lengths of exons from the graphics alone. In Figure 11, exons are displayed using one linear scale, while introns are displayed as log (length).) (Comment on Figure 14: The sequences of Figure 12, as displayed using a single base scale for all introns and exons.)

Please amend paragraph [0056] beginning on page 10 as follows:

The representation technique can be used for circular genomes, such as bacterial genomes, as well, with the effect of altering the length of the arc of the circle for each subsequence. (Figure 15.) (Comment on Figure 15: Regions in black are displayed using one scale, while regions in white are displayed in another. The effect is to alter the relative sizes of the areas allocated to different annotations.)

Please amend paragraph [0058] beginning on page 10 as follows:

In one embodiment, the gene product representation technique combines gene product expression data with a genome browser or splice graph view of the gene product sequences. The representation technique indicates the expression level of a gene product, or region of a gene product, in the view in a graphical way. In one embodiment, it varies the color saturation of a portion of the gene product representation according to the expression level. The gene product representation may consist of a geometric shape, a text string, or a symbol, e.g., it may consist of multiple regions whose expression levels have been measured independently. (Figures 16 and 17.) (Comment on Figure 16: Exons 13 through 16 of gene ZC1. Three alternately spliced forms are depicted across the region comprising exons 14 and 15. Exons 13 and 16 are filled with solid black, indicating one expression level, equal to the gene expression. The alternately spliced forms, labeled V1, V2 and V3, must each have an expression level less than or equal to the gene expression. In the figure, V1 (variant one) is filled with white (fully desaturated) to indicate an expression level of zero (not expressed). Variant two (V2) is filled with gray (partial saturation of the color black) to indicate expression greater than zero but less than the gene expression level. By inference, variant three (V3) accounts for the remainder of the expression. Its expression level could be displayed by a solid shape filled with gray.) (Comment on Figure 17: Variant one (V1) is not expressed, while variants two and three (V2 and V3) are expressed in approximately equal quantities. White = not expressed, Black = gene expression.)

Please amend paragraph [0059] beginning on page 10 as follows:

In another embodiment, the representation technique indicates the expression level by varying the color of a portion of the gene product representation. In another embodiment, the representation technique indicates the expression level by varying the "fill" of a portion of the gene product representation. In another embodiment, the representation technique indicates the expression level by varying the hue of a portion of the gene product representation. In another embodiment, the representation technique indicates the expression level by varying the brightness of a portion of the gene product

representation. In another embodiment, the representation technique indicates the expression level by varying the transparency of a portion of the gene product representation. In another embodiment, the representation technique indicates the expression level by varying the size of the gene product representation. In another embodiment, the representation technique indicates the expression level through a combination of saturation, fill, hue, brightness, transparency and size. (Figure 18.) (Comments on Figure 18: The middle exon is "filled" proportional to its expression level. The size (vertically) of the middle exon indicate its relative expression level.)

Please amend paragraph [0060] beginning on page 11 as follows:

To display expression levels from more than two samples in the same display, the representation technique, in one embodiment, uses a different color for each sample. For example, if the expression level is greater in sample one than in sample two, the color might be green; if the expression level is greater in sample two than in sample one, the color might be red. If it is equal, the color might be white. (Figure 19B.) (Comment on Figure 19(B): Samples one and two are shown in different colors. Exon 2 (E2) is differentially expressed. In sample one (green), variant one (V1) is more highly expressed. In sample two (red), variant two (V2) is more highly expressed. Exons one and three (E1 & E3) are equally expressed in the two samples (indicated with white).)

Please amend paragraph [0061] beginning on page 11 as follows:

In another embodiment, the representation technique displays expression from two or more samples by allocating a portion of the gene product representation for each sample and independently varying the attributes of that portion. The color of each portion could be the same (e.g., green) or different (e.g., green for sample one, red for sample two). In one embodiment, the gene product representation is split horizontally into two portions; in the top portion, the expression level in sample one is displayed, and in the bottom portion, the expression level in sample two. The attributes within each portion are varied based on the expression level of the sample corresponding to that portion. (Figure

19A.) (Comment on Figure 19(A): The bar representing each exon is split in half, with each half used to display the expression level of one sample. In this example, V1 of exon 2 (E2) is more highly expressed in sample one (the top half of the bar), while variant two (V2) of exon 2 is more highly expressed in sample two (the bottom half of the bar). Exons 1 and 3 are equally expressed in both samples.)

Please amend paragraph [0062] beginning on page 11 as follows:

In another embodiment, the relative size of the portions is modified to indicate changes in expression level. In another embodiment, the representation technique displays more than two tissues by splitting a gene product representation into additional portions. (Comment on Figure 20A: A hypothetical hierarchical cluster of three genes (Gene 1, Gene 2 and Gene 3) and their variants. Each node has a rectangular label. The label's color saturation indicates the expression level. In this example, gene two variants one and three are not expressed (indicated with white), while gene two variant two (Gene 2, V2) is expressed (indicated with gray). Gene one, variant two is expressed more highly than variant one (indicated with a darker, more saturated gray). (Comment on Figure 20B: Relative expression levels are indicated by the size of the circle shown at each node.) (Comment on Figure 21(A): Gene one is more highly expressed in sample two (shown in red), gene two is more highly expressed in sample one (indicated with green), while gene 3 is equally expressed in the two samples.) (Comment on Figure 21(B): Portions of the display area are allocated to indicate relative expression, such as the ratio between two samples.) (Comment on Figure 21(C): The display area for each protein is split. In each portion, expression in one sample is shown with a color and a saturation. Protein 3 is not expressed in either sample; protein 1 more highly in sample 2 (red); and protein 2, more highly in sample one (green).)